



SEQUENCE LISTING

<110> STRACKE, MARY  
LIOTTA, LANCE  
SCHIFFMANN, ELLIOTT  
KRUTZCH, HENRY  
MURATA, JUN

<120> AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN  
CANCER DIAGNOSIS AND THERAPY

<130> 2026-4149US4

<140> 09/483,831

<141> 2000-01-17

<150> 07/822,043

<151> 1992-01-17

<150> 08/249,182

<151> 1994-05-25

<150> 08/346,455

<151> 1994-11-28

<150> 08/977,221

<151> 1997-11-24

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<170> PatentIn Ver. 2.1

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Primers

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<210> 26

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Peptide

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Gln Tyr Leu His Gln Tyr Gly Ser Ser

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<210> 27

<211> 5

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<223> Description of Artificial Sequence: Synthetic  
Peptide

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Val Leu Asn Tyr Phe

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<210> 28

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
Peptide

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Tyr Leu Asn Ala Thr

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<210> 29

<211> 11

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Peptide

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Peptide

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His Asp Thr Glu Asp Lys  
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<213> Homo sapiens

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<223> Putative protein sequence of A2058 Autotoxin

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Cys His Asp Phe Asp Glu Leu Cys Leu Lys Thr Ala Arg Gly Trp Glu  
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His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr	Asn	Tyr	35	40	45
Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp	Val	Asp	Asp	Asp	Cys	Glu	50	55	60
Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly	Phe	Val	Arg	Pro	Pro	Leu	65	70	75
Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala	Ser	Tyr	Met	Lys	Lys	Gly	85	90	95
Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu	Arg	Ser	Cys	Gly	Thr	His	100	105	110
Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	115	120	125
Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly	130	135	140
Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	Thr	Phe	His	Leu	Arg	Gly	145	150	155
Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	Gly	Gln	Pro	Leu	Trp	Ile	165	170	175
Thr	Ala	Thr	Lys	Gln	Gly	Val	Lys	Ala	Gly	Thr	Phe	Phe	Trp	Ser	Val	180	185	190
Val	Ile	Pro	His	Glu	Arg	Arg	Ile	Leu	Thr	Ile	Leu	Arg	Trp	Leu	Thr	195	200	205
Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	210	215	220
Pro	Asp	Phe	Ser	Gly	His	Lys	Tyr	Gly	Pro	Phe	Gly	Pro	Glu	Glu	Ser	225	230	235
Ser	Tyr	Gly	Ser	Pro	Phe	Thr	Pro	Ala	Lys	Arg	Pro	Lys	Arg	Lys	Val	245	250	255
Ala	Pro	Lys	Arg	Arg	Gln	Glu	Arg	Pro	Val	Ala	Pro	Pro	Lys	Lys	Arg	260	265	270

18

D

Asp	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	Lys	530	535	540
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Arg	His	Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr	565	570	575
Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	Ile	Phe	580	585	590
Leu	Met	Leu	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	Glu	Val	595	600	605
Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg	610	615	620
Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys	625	630	635
Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro	645	650	655
Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr	660	665	670
Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu	Val	Lys	675	680	685
Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn	Val	Ile	Ser	Gly	Pro	Ile	690	695	700
Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys	Ile	Lys	705	710	715
Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr	Tyr	Ser	725	730	735
Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln	Pro	Ala	Asp	Lys	Cys	Asp	740	745	750
Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile	Leu	Pro	His	Arg	Pro	Asp	Asn	755	760	765
Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val	Glu	Glu	770	775	780

Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr  
785 790 795 800

Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
805 810 815

Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile  
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<213> Homo sapiens

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<223> Partial DNA sequence of A2058 Autotoxin

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<210> 36

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Cys Gly Glu Val Arg Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp
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Cys Leu Ala Arg Gly Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys
      50              55              60

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```

Gly Glu Ser His Trp Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala
      65              70              75              80

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Glu Cys Leu Gln Val Asp Ser Pro Ser Ile Asn His Leu Leu Arg Gly

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79

D

85					90					95						
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100					105					110						
Asn	Ile	Glu	Lys	Leu	Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	
115					120					125						
Pro	Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	
130					135					140						
Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	
145					150					155					160	
Pro	Val	Phe	Asp	Ala	Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	
165					170					175						
His	Arg	Trp	Trp	Ala	Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	
180					185					190						
Arg	Gly	Glu	Ser	Trp	Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	
195					200					205						
Ala	Glu	Ile	Leu	Thr	Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	
210					215					220						
Arg	Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly	
225					230					235					240	
His	Lys	His	Met	Pro	Phe	Gly	Pro	Glu	Met	Pro	Asn	Pro	Leu	Arg	Glu	
245					250					255						
Met	His	Lys	Ile	Val	Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	
260					265					270						
Leu	His	Arg	Cys	Val	Asn	Val	Ile	Phe	Val	Glu	Thr	Met	Asp	Gly	Arg	
275					280					285						
Cys	His	Met	Tyr	Arg	Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	
290					295					300						
Asp	Asp	Ile	Thr	Leu	Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	
305					310					315					320	
Phe	Ser	Asn	Asn	Ala	Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	
325					330					335						
Thr	Cys	Lys	Lys	Pro	Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	

340 345 350  
 Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile  
 355 360 365  
 His Leu Leu Val Glu Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp  
 370 375 380  
 Val Tyr Lys Lys Pro Ser Gly Asn Ala Phe Ser Arg Glu Thr Thr Ala  
 385 390 395 400  
 Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly  
 405 410 415  
 Pro Thr Phe Lys Tyr Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu  
 420 425 430  
 Leu Tyr Asn Val Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn  
 435 440 445  
 Asn Gly Thr His Phe Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe  
 450 455 460  
 Arg Pro Thr Met Pro Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile  
 465 470 475 480  
 Met Tyr Leu Gln Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys  
 485 490 495  
 Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr  
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 Lys Gly Ser Thr Glu Glu Arg His Leu Leu Tyr Gly Asp Arg Pro Ala  
 515 520 525  
 Val Leu Tyr Arg Thr Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu  
 530 535 540  
 Ser Gly Tyr Ser Glu Ile Phe Leu Met Pro Leu Trp Thr Ser Tyr Thr  
 545 550 555 560  
 Val Ser Lys Gln Ala Glu Val Ser Ser Val Pro Asp His Leu Thr Ser  
 565 570 575  
 Cys Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys  
 580 585 590  
 Leu Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Gly Leu Gly Pro

595		600		605
Pro Tyr Leu Ser Ser Ser	Pro Glu Ala Lys Tyr Asp	Ala Phe Leu Val		
610	615	620		
Thr Asn Met Val Pro Met Tyr	Pro Ala Phe Lys Arg Val	Trp Asn Tyr		
625	630	635	640	
Phe Gln Arg Val Leu Val Lys	Lys Tyr Ala Ser Glu Arg	Asn Gly Val		
645	650	655		
Asn Val Ile Ser Gly Pro Ile	Phe Asp Tyr Asp Tyr Asp	Gly Leu His		
660	665	670		
Asp Thr Glu Asp Lys Ile Lys	Gln Tyr Val Glu Gly Ser	Ser Ile Pro		
675	680	685		
Val Pro Thr His Tyr Tyr Ser	Ile Ile Thr Ser Cys Leu	Asp Phe Thr		
690	695	700		
Gln Pro Ala Asp Lys Cys Asp	Gly Pro Leu Ser Val Ser	Ser Phe Ile		
705	710	715	720	
Leu Pro His Arg Pro Asp Asn	Glu Glu Ser Cys Asn Ser	Ser Glu Asp		
725	730	735		
Glu Ser Lys Trp Val Glu Glu	Leu Met Lys Met His Thr	Ala Arg Val		
740	745	750		
Arg Asp Ile Glu His Leu Thr	Ser Leu Asp Phe Phe Arg	Lys Thr Ser		
755	760	765		
Arg Ser Tyr Pro Glu Ile Leu	Thr Leu Lys Thr Tyr Leu	His Thr Tyr		
770	775	780		
Glu Ser Glu Ile				
785				

<210> 37

<211> 2712

<212> DNA

<213> Homo sapiens

<220>

<223> N-tera 2D1 ATX DNA sequence

<400> 37



DS  
Conf

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aatgcctgtc actgctcaga ggactgcttg gccaggggag actgctgtaa caattaccaa 180  
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<212> PRT  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: Synthetic  
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<400> 38  
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<210> 39  
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<210> 40  
<211> 8  
<212> PRT  
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<400> 40  
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<210> 41  
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<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 41

Val Met Pro Asn Ile Glu Lys

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5

<210> 42

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<400> 42

Thr Ala Arg Gly Trp Glu Cys Thr

1

5

<210> 43

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Peptide

<220>

<221> VARIANT

<222> (1)

<223> Xaa represents either an unknown or any amino acid residue.

<220>

<221> VARIANT

<222> (7)

<400> 43

Xaa Asp Ser Pro Trp Thr Xaa Ile Ser Gly Ser

1

5

10

<210> 44  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 44  
Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met  
1 5 10

<210> 45  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 45  
Thr Tyr Leu His Thr Tyr Glu Ser  
1 5

<210> 46  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 46  
Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp Gln  
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<210> 47  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 47

Ile Val Gly Gln Leu Met Asp Gly  
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<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 48

Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
1 5

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 49

Gln Ala Glu Val Ser Ser Val Pro Asp  
1 5

<210> 50

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 50

Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro Asp Asp Cys  
1 5 10

<210> 51  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 51  
Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu  
1 5 10

<210> 52  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

<400> 52  
Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro  
1 5 10 15

<210> 53  
<211> 117  
<212> DNA  
<213> Homo sapiens

<220>  
<223> 5' end of human liver ATX gene

<400> 53  
atggcaagga ggagctcggt ccagtcgtgt caagatatat ccctgttcac ttttgccggt 60  
ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgg 117

<210> 54  
<211> 39  
<212> PRT  
<213> Homo sapiens

<220>

<223> N-terminal region including transmembrane domain  
of liver ATX protein

<400> 54

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe  
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg  
20 25 30

Ile Lys Arg Ala Glu Gly Trp  
35

<210> 55

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 55

gctcagataa ggaggaaaga g

21

<210> 56

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 56

gaatccgtag gacatctgct t

21

<210> 57

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 57  
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21

<210> 58  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

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<223> Base y represents t/u or c.

<220>  
<221> variation  
<222> (6)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (12)  
<223> Base r represents g or a.

<220>  
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<222> (15)  
<223> Base n represents inosine.

<220>  
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<222> (18)  
<223> Base n represents inosine.

<220>  
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<222> (21)  
<223> Base y represents c or t/u.

<220>  
<221> variation  
<222> (24)



<223> Base n represents inosine.

<400> 58

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25

OS  
cont.  
<210> 59

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (6)

<223> Base n represents inosine..

<220>

<221> variation

<222> (9)

<223> Base n represents inosine.

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<223> Base y represents c or t/u.

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<221> variation

<222> (15)

<223> Base n represents inosine.

<220>

<221> variation

<222> (18)

<223> Base n represents inosine.

<220>

<221> variation

<222> (21)

<223> Base n represents inosine.

<220>

<221> variation

<222> (24)

<223> Base y represents c or t/u.

<400> 59

ttygtnggnt ayggncnac nttyaa

26

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Basen y represents c or t/u.

<220>

<221> variation

<222> (6)

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<220>

<221> variation

<222> (9)

<223> Base n represents inosine.

<220>

<221> variation

<222> (12)

<223> Base n represents inosine.

<220>

<221> variation

<222> (15)

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<220>

<221> variation

<222> (18)

<223> Base n represents inosine.

<220>

<221> variation

<222> (21)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (24)

<223> Base y represents c or t/u.

<400> 60

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26

<210> 61

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (6)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (9)

<223> Base n represents inosine.

<220>

<221> variation

<222> (12)

<223> Base n represents inosine.

<220>

<221> variation

<222> (15)

<223> Base n represents inosine.

<220>

<221> variation

<222> (18)

<223> Base n represents inosine..

<220>

<221> variation

<222> (21)

<223> Base n represents inosine.

<220>

<221> variation

<222> (24)

<223> Base n represents inosine.

<400> 61

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26

<210> 62

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<221> variation

<222> (3)

<223> Base y represents t/u or c.

<220>

<221> variation

<222> (6)

<223> Base y represents c or t/u.

<220>

<221> variation

<222> (9)..(10)

<223> Base r represents a or g. Base y represents c  
or t/u.

<220>

<221> variation

<222> (12)  
<223> Base n represents inosine.

<220>  
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<222> (15)  
<223> Base r represents a or g.

<220>  
<221> variation  
<222> (18)  
<223> Base r represents a or g.

<220>  
<221> variation  
<222> (21)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (24)  
<223> Base n represents inosine.

<220>  
<221> variation  
<222> (27)  
<223> Base n represents inosine.

<400> 62  
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29

<210> 63  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Putative autotoxin protein sequence from human  
liver

<220>  
<221> VARIANT  
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<223> Xaa at positions: 860, 889, 905, 911, 927, 937,  
944, 950, 954, 967, 975 represents either an  
unknown or any amino acid residue.

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 63

gctgtcttca aacacagc

18

<210> 64

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 64

ctgggtggctg taatccatag c

21

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 65

cgtgaaggca aagagaacac g

21

<210> 66

<211> 3104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Polynucleotide

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gagtcaatat ctgcttagga ttcactgcac atcgaattaa gagagcagaa ggatgggagg 180  
aaggtcctcc tacagtgcta tcagactccc cctggaccaa catctccgga tcttgcaagg 240

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cagaggactg	cttggccagg	ggagactgct	gtaccaatta	ccaagtgggt	tgcaaaggag	480
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gcatgcagac	tgtttttgta	ggttatggcc	caacatttaa	gtacaagact	aaagtgcctc	1560
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ctaataatgg	gacctatgga	agtttgaatc	atctcctgcg	cactaatacc	ttcaggccaa	1680
ccatgccaga	ggaagttacc	agaccaatt	atccagggat	tatgtacctt	cagtctgatt	1740
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gccgcagcta	cccagaaatc	ctgacactca	agacatacct	gcatacatat	gagagcgaga	2640
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gccttggtgt	ctgagtagag	cttgtaataa	atactgcagc	ttgagtthtt	agtggagact	2880
tctaaatggg	gctgcagatt	tgatatttgc	attgaggaaa	tattaattth	ccaatgcaca	2940
gttgccacat	ttagtcctgt	actgtatgga	aacactgatt	ttgtaaagtt	gcctthattt	3000
gctgttaact	gttaactatg	acagatatat	ttaagcctta	taaaccaatc	ttaaacataa	3060
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<210> 67

<211> 861

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Polypeptide

<400> 67

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Ile	Ile	Ser	Leu	Phe
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Thr	Phe	Ala	Val	Gly	Val	Asn	Ile	Cys	Leu	Gly	Phe	Thr	Ala	His	Arg
			20					25					30		
Ile	Lys	Arg	Ala	Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser
		35					40						45		
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys	Gly	Arg	Cys	Phe
		50				55					60				
Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro	Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys
65					70					75				80	
Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
				85					90					95	
Thr	Ala	Arg	Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg
			100					105					110		
Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly
		115					120					125			
Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
		130				135					140				
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly
145					150					155				160	
Phe	Val	Arg	Pro	Pro	Leu	Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala
				165					170					175	
Ser	Tyr	Met	Lys	Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu
			180					185					190		



Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	His	Met	Arg	Pro	Val	Tyr	Pro	Thr	195	200	205	
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	210	215	220	
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	225	230	235	240
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly	245	250	255	
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp	260	265	270	
Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr	275	280	285	
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Leu	Arg	Ser	Met	290	295	300	
Pro	Ser	Ile	Leu	Ser	Asn	Leu	Ile	Ser	Leu	Asp	Thr	Asn	Met	Pro	Phe	305	310	315	320
Gly	Pro	Glu	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	Asp	Lys	Ile	Val	Gly	325	330	335	
Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys	Val	Asn	340	345	350	
Val	Ile	Phe	Val	Gly	Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp	Arg	355	360	365	
Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	370	375	380	
Val	Pro	Gly	Thr	Leu	Gly	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys	385	390	395	400
Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp	405	410	415	
Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	His	420	425	430	
Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	Arg	435	440	445	

Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser	
450						455					460					
Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	Phe	Asp	Asn	Lys	Val	Asn	
465					470					475					480	
Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys	
				485					490					495		
Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys	
			500					505					510			
Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	Ser	
		515					520					525				
Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu	
	530					535					540					
Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp	
545					550					555					560	
Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	Lys	
				565					570					575		
Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu	Glu	
			580					585					590			
Arg	His	Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr	
		595					600					605				
Asp	Val	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	Ile	Phe	
	610					615					620					
Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	Glu	Val	
625					630					635					640	
Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg	
				645					650					655		
Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys	
			660					665					670			
Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro	
		675					680					685				
Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr	
	690					695					700					

Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys  
705 710 715 720

Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly Pro Ile  
725 730 735

Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys  
740 745 750

Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser  
755 760 765

Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp  
770 775 780

Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Arg His Arg Pro Asp Asn  
785 790 795 800

Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu  
805 810 815

Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr  
820 825 830

Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
835 840 845

Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile  
850 855 860

<210> 68

<211> 3251

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Polynucleotide

<400> 68

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ctgcttagga ttcactgcac atcgaattaa gagagcagaa ggatgggagg aaggtcctcc 180  
tacagtgcta tcagactccc cctggaccaa catctccgga tcttgcaagg gcaggtgctt 240  
tgaacttcaa gaggctggac ctcttgattg tcgctgtgac aacttgtgta agagctatac 300  
cagttgctgc catgactttg atgagctgtg tttgaagaca gcccgtggct gggagtgtac 360  
taaggacaga tgtggagaag tcagaaatga agaaaatgcc tgtcactgct cagaggactg 420

cttggccagg ggagactgct gtaccaatta ccaagtgggt tgcaaaggag agtcgcattg 480  
 ggttgatgat gactgtgagg aaataaaggc cgcagaatgc cctgcagggt ttgttcgccc 540  
 tccattaatc atcttctccg tggatggctt ccgtgcatca tacatgaaga aaggcagcaa 600  
 agtcatgcct aatattgaaa aactaagggtc ttgtggcaca cactctccct acatgaggcc 660  
 ggtgtaccca actaaaacct ttcctaactt atacactttg gccactgggc tatatccaga 720  
 atcacatgga attgttggca attcaatgta tgatcctgta tttgatgcca cttttcatct 780  
 gcgagggcga gagaaattta atcatagatg gtggggagggt caaccgctat ggattacagc 840  
 caccaagcaa ggggtgaaag ctggaacatt cttttgggtc gttgtcatcc ctcacgagcg 900  
 gagaatatta accatattgc ggtggctcac cctgccagat catgagaggc cttcggtcta 960  
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 ggagagtagt tatggctcac cttttactcc ggctaagaga cctaagagga aagttgcccc 1080  
 taagaggaga caggaaagac cagttgctcc tccaaagaaa agaagaagaa aaatacatag 1140  
 gatggatcat tatgctgcgg aaactcgtca ggacaaaatg acaaatcctc tgaggggaaat 1200  
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 aattcgatcc aaatttagca acaatgctaa atatgacccc aaagccatta ttgccaatct 1440  
 cacgtgtaaa aaaccagatc agcactttaa gccttacttg aaacagcacc ttcccaaacg 1500  
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 agaagagaga cacctcctct atgggcgacc tgcagtgctt tatcggacta gatatgatat 2040  
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 cattgaggaa atattaatth tccaatgcac agttgccaca tttagtcttg tactgtatgg 3120  
 aaacactgat tttgtaaagt tgcctttatt tgctgttaac tgttaactat gacagatata 3180  
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 aaaaaaaaaa a 3251

PS  
 Conf

<210> 69  
<211> 915  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Polypeptide

<400> 69

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Thr	Phe	Ala	Val	Gly	Val	Ser	Ile	Cys	Leu	Gly	Phe	Thr	Ala	His	Arg	
			20					25					30			
Ile	Lys	Arg	Ala	Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser	
		35					40						45			
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys	Gly	Arg	Cys	Phe	
	50					55					60					
Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro	Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys	
65					70					75				80		
Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys	
				85					90					95		
Thr	Ala	Arg	Gly	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg	
			100					105					110			
Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly	
			115				120					125				
Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp	
	130					135					140					
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly	
145					150					155				160		
Phe	Val	Arg	Pro	Pro	Leu	Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala	
				165					170					175		
Ser	Tyr	Met	Lys	Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu	
			180					185					190			

Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg Pro Val Tyr Pro Thr  
 195 200 205

Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu  
 210 215 220

Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala  
 225 230 235 240

Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp Gly  
 245 250 255

Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln Gly Val Lys Ala Gly  
 260 265 270

Thr Phe Phe Trp Ser Val Val Ile Pro His Glu Arg Arg Ile Leu Thr  
 275 280 285

Ile Leu Arg Trp Leu Thr Leu Pro Asp His Glu Arg Pro Ser Val Tyr  
 290 295 300

Ala Phe Tyr Ser Glu Gln Pro Asp Phe Ser Gly His Lys Tyr Gly Pro  
 305 310 315 320

Phe Gly Pro Glu Glu Ser Ser Tyr Gly Ser Pro Phe Thr Pro Ala Lys  
 325 330 335

Arg Pro Lys Arg Lys Val Ala Pro Lys Arg Arg Gln Glu Arg Pro Val  
 340 345 350

Ala Pro Pro Lys Lys Arg Arg Arg Lys Ile His Arg Met Asp His Tyr  
 355 360 365

Ala Ala Glu Thr Arg Gln Asp Lys Met Thr Asn Pro Leu Arg Glu Ile  
 370 375 380

Asp Lys Ile Val Gly Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu  
 385 390 395 400

Arg Arg Cys Val Asn Val Ile Phe Val Gly Asp His Gly Met Glu Asp  
 405 410 415

Val Thr Cys Asp Arg Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val  
 420 425 430

Asp Asp Ile Thr Leu Val Pro Gly Thr Leu Gly Arg Ile Arg Ser Lys  
 435 440 445

104

0

Phe Ser Asn Asn Ala Lys Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu  
 450 455 460

Thr Cys Lys Lys Pro Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His  
 465 470 475 480

Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile  
 485 490 495

His Leu Leu Val Glu Arg Arg Trp His Val Ala Arg Lys Pro Leu Asp  
 500 505 510

Val Tyr Lys Lys Pro Ser Gly Lys Cys Phe Phe Gln Gly Asp His Gly  
 515 520 525

Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly  
 530 535 540

Pro Thr Phe Lys Tyr Lys Thr Lys Val Pro Pro Phe Glu Asn Ile Glu  
 545 550 555 560

Leu Tyr Asn Val Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn  
 565 570 575

Asn Gly Thr His Gly Ser Leu Asn His Leu Leu Arg Thr Asn Thr Phe  
 580 585 590

Arg Pro Thr Met Pro Glu Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile  
 595 600 605

Met Tyr Leu Gln Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys  
 610 615 620

Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys Arg Leu His Thr  
 625 630 635 640

Lys Gly Ser Thr Glu Glu Arg His Leu Leu Tyr Gly Arg Pro Ala Val  
 645 650 655

Leu Tyr Arg Thr Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu Ser  
 660 665 670

Gly Tyr Ser Glu Ile Phe Leu Met Leu Leu Trp Thr Ser Tyr Thr Val  
 675 680 685

Ser Lys Gln Ala Glu Val Ser Ser Val Pro Asp His Leu Thr Ser Cys  
 690 695 700

Val Arg Pro Asp Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys Leu  
705 710 715 720

Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro  
725 730 735

Tyr Leu Ser Ser Ser Pro Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr  
740 745 750

Asn Met Val Pro Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe  
755 760 765

Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn  
770 775 780

Val Ile Ser Gly Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp  
785 790 795 800

Thr Glu Asp Lys Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val  
805 810 815

Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln  
820 825 830

Pro Ala Asp Lys Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile Leu  
835 840 845

Pro His Arg Pro Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu  
850 855 860

Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg  
865 870 875 880

Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg  
885 890 895

Ser Tyr Pro Glu Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu  
900 905 910

Ser Glu Ile  
915

<210> 70

<211> 979

<212> PRT

<213> Homo sapiens



<220>

<223> Putative autotoxin protein sequence from human liver.

<220>

<221> VARIANT

<222> (860)

<223> Xaa at positions: 860, 889, 905, 911, 927, 937, 944, 950, 954, 967, and 975 represents an unknown or other amino acid.

<400> 70

Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp Ile Ser Leu Phe  
1 5 10 15

Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg  
20 25 30

Ile Lys Arg Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser  
35 40 45

Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe  
50 55 60

Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys  
65 70 75 80

Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys  
85 90 95

Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg  
100 105 110

Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly  
115 120 125

Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp  
130 135 140

Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Leu Gln Val  
145 150 155 160

Cys Ser Pro Ser Ile Asn His Leu Leu Arg Gly Trp Leu Pro Met Thr  
165 170 175

Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu  
180 185 190

Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro	Thr
195				200				205							
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu
210				215				220							
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala
225				230				235				240			
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly
				245				250				255			
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp
				260				265				270			
Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr
275				280				285							
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val	Tyr
290				295				300							
Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly	His	Lys	His	Met	Pro
305				310				315				320			
Phe	Gly	Pro	Glu	Met	Thr	Asn	Pro	Leu	Arg	Glu	Met	His	Lys	Ile	Val
				325				330				335			
Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys	Val
340				345				350							
Asn	Val	Ile	Phe	Val	Glu	Thr	Met	Asp	Gly	Arg	Cys	His	Met	Tyr	Arg
355				360				365							
Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu
370				375				380							
Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala
385				390				395				400			
Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro
405				410				415							
Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu
420				425				430							
His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu
435				440				445							

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Arg	Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	450	455	460	
Ser	Gly	Asn	Ala	Phe	Ser	Arg	Glu	Thr	Thr	Ala	Phe	Asp	Asn	Lys	Val	465	470	475	480
Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	485	490	495	
Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	500	505	510	
Cys	Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	515	520	525	
Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	530	535	540	
Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	545	550	555	560
Asp	Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	565	570	575	
Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu	580	585	590	
Glu	Arg	His	Leu	Leu	Tyr	Gly	Asp	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	595	600	605	
Arg	Tyr	Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	610	615	620	
Ile	Phe	Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	625	630	635	640
Glu	Val	Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	645	650	655	
Val	Arg	Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	660	665	670	
Asp	Lys	Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	675	680	685	
Ser	Pro	Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	690	695	700	

Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu  
705 710 715 720

Val Lys Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly  
725 730 735

Pro Ile Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys  
740 745 750

Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr  
755 760 765

Tyr Ser Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys  
770 775 780

Cys Asp Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Pro His Arg Pro  
785 790 795 800

Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val  
805 810 815

Glu Glu Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His  
820 825 830

Leu Thr Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu  
835 840 845

Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile Xaa  
850 855 860

Leu Ser Glu His Leu Gln Tyr Ser Leu Ile Asn Trp Leu Tyr Ile Phe  
865 870 875 880

Ile Leu Phe Leu Tyr Leu Leu Ile Xaa Asn Gln Asp Ile Lys Asn Val  
885 890 895

Ser Ile Leu Ile Leu Tyr Gln Ile Xaa His Ile Met Pro Glu Xaa Leu  
900 905 910

His Cys Phe Ser Leu Met Leu Asp Leu Gly Ser Leu Val Phe Xaa Val  
915 920 925

Glu Leu Val Ile Asn Thr Ala Ala Xaa Val Phe Ser Gly Ser Phe Xaa  
930 935 940

Met Val Leu Gln Ile Xaa Tyr Leu His Xaa Gly Asn Ile Asn Phe Pro  
945 950 955 960

Met His Ser Cys His Ile Xaa Ser Cys Thr Val Trp Lys His Xaa Phe  
965 970 975

Cys Lys Val

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